

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2003, 10:33:25 ; Search time 2192 Seconds
(without alignments)
12279.607 Million cell updates/sec

Title: US-10-037-311A-2

Perfect score: 1662

Sequence: 1 atgagcagaattcgtagcag.....gggggaacttaagctagtatga 1662

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	481.4	29.0	483	9 AI994677	AI994677 701499231
2	440.8	26.5	559	14 R90192	R90192 16547 Lambd
3	331	19.9	416	10 AV805720	AV805720 AV805720
4	309.6	18.6	668	17 B77193	B77193 T31J1TR TAM
5	296	17.8	507	9 AA605483	AA605483 30519 Lam
6	281	16.9	645	10 BE319670	BE319670 NF017D12R

7	280	16.8	597	13	BI416307	BI416307 LJNEST4b4
8	272	16.4	443	10	AV807820	AV807820 AV807820
9	259.8	15.6	559	10	AW719438	AW719438 LJNEST4f1
10	259.6	15.6	671	17	B23728	B23728 F16M20TR IG
11	252.6	15.2	508	12	BF597909	BF597909 sv02f04.y
12	250.2	15.1	561	12	BF009322	BF009322 ss76g10.y
13	245.2	14.8	605	10	BE346170	BE346170 sp19b08.y
14	235.6	14.2	314	10	AV831440	AV831440 AV831440
15	232.4	14.0	786	17	BI8679	BI8679 F16A14-T7 I
16	224.4	13.5	535	12	BG356747	BG356747 OV2_9.E02
17	209.2	12.6	505	12	BG045011	BG045011 saa36d05.
18	205.4	12.4	552	13	BI969461	BI969461 GM8300008A
19	199.2	12.0	658	10	AW693268	AW693268 NF064A03S
20	198.8	11.9	592	17	BH555955	BH555955 BOHFU09TR
21	188.8	11.4	570	13	BI425718	BI425718 sab71b08.
22	187	11.3	404	17	BH862014	BH862014 SALK_0885
23	187	11.3	594	12	BE802468	BE802468 sr31f08.y
24	181.2	10.9	470	13	BI969504	BI969504 GM8300008A
25	178.2	10.7	597	13	BI946374	BI946374 O1117 lea
26	178	10.7	380	10	BE662954	BE662954 EST00099
27	172	10.3	418	14	BQ985962	BQ985962 OGE8D08.y
28	172	10.3	430	14	BQ980670	BQ980670 QGE11L07.
29	172	10.3	448	14	BQ990773	BQ990773 QGF21B03.
30	172	10.3	465	14	BQ873962	BQ873962 QG14A14.y
31	170.4	10.3	373	14	BQ984710	BQ984710 QGE4e05.y
32	168.4	10.1	562	13	BM525521	BM525521 sal28h09.
33	161.8	9.7	613	10	BE361458	BE361458 DG1_72_E0
34	159.4	9.6	649	10	AV836113	AV836113 AV836113
35	158.6	9.5	992	10	BE040029	BE040029 OC10F08 O
36	151.6	9.1	323	17	AZ130387	AZ130387 OSJNB010
37	150.8	9.1	740	12	BE823653	BE823653 GM700021A
38	149.8	9.0	812	17	BH495933	BH495933 BOHNS54TF
39	142.4	8.6	301	17	AQ796429	AQ796429 nbxb0066A
40	142	8.5	415	10	AW704030	AW704030 SK27a04.y
41	141.4	8.5	529	12	BG357064	BG357064 OV2_9.E02
42	140.8	8.5	663	13	BJ314543	BJ314543 BJ314543
43	140.2	8.4	564	10	AW720399	AW720399 LJNEST22C
44	139.6	8.4	377	17	BH548166	BH548166 BQGW62TR
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ALIGNMENTS

RESULT 1	AI994677	701499231	A. thaliana, Ohio State clone set	483 bp	mRNA	linear	EST 08-SEP-1999
LOCUS	AI994677	701499231	A. thaliana, Ohio State clone set	483 bp	mRNA	linear	EST 08-SEP-1999
DEFINITION	AI994677	701499231	A. thaliana, Ohio State clone set	483 bp	mRNA	linear	EST 08-SEP-1999
ACCESSION	AI994677	701499231	A. thaliana, Ohio State clone set	483 bp	mRNA	linear	EST 08-SEP-1999
VERSION	AI994677	701499231	A. thaliana, Ohio State clone set	483 bp	mRNA	linear	EST 08-SEP-1999
KEYWORDS	AI994677	701499231	A. thaliana, Ohio State clone set	483 bp	mRNA	linear	EST 08-SEP-1999
SOURCE	AI994677	701499231	A. thaliana, Ohio State clone set	483 bp	mRNA	linear	EST 08-SEP-1999
ORGANISM	AI994677	701499231	A. thaliana, Ohio State clone set	483 bp	mRNA	linear	EST 08-SEP-1999
REFERENCE	AI994677	701499231	A. thaliana, Ohio State clone set	483 bp	mRNA	linear	EST 08-SEP-1999
AUTHORS	AI994677	701499231	A. thaliana, Ohio State clone set	483 bp	mRNA	linear	EST 08-SEP-1999
TITLE	AI994677	701499231	A. thaliana, Ohio State clone set	483 bp	mRNA	linear	EST 08-SEP-1999
JOURNAL	AI994677	701499231	A. thaliana, Ohio State clone set	483 bp	mRNA	linear	EST 08-SEP-1999
COMMENT	AI994677	701499231	A. thaliana, Ohio State clone set	483 bp	mRNA	linear	EST 08-SEP-1999

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/db_xref="taxon:3702"
/clone="70149231"
/clone_lib="A. thaliana, Ohio State clone set"
/note="cDNA library was made from selected clones from the Arabidopsis thaliana Ohio State clone set."
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Matches 482; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 805 GGAGATCATGATAAGATGTTCTTCTGTGAAGGAGACCAACATTCATCGGGAAGTCCCT 864
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DB 1 GGAGATCATGATAAGATGTTCTTCTGTGAAGGAGACCAACATTCATCGGGAAGTCCCT 60
QY 865 TCGTTGATGTTTAAACAGACAATFACATTTGTTCCATCTCTGTGGTTAATACGGGTTTC 924
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DB 61 TGGTTGATGTTTAAACAGACAATFACATTTGTTCCATCTCTGTGGTTAATACGGGTTTC 120
QY 925 GATGATGAACAAAGCTATTCACAGAAAGCGGCTGCTTTCATCAGTATAGTAGG 984
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DB 121 GATGATGAACAAAGCTATTCACAGAAAGCGGCTGCTTTCATCAGTATAGTAGG 180
QY 985 TATCTTTTTCACCAACTAATCCAAAGTATGGGCTTAGTCAGTATAGTACGAGGTTAC 1044
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DB 161 TATCTTTTTCACCAACTAATCCAAAGTATGGGCTTAGTCAGTATAGTACGAGGTTAC 240
QY 1045 TTATCGATCGGGATGAGAGATTTGGGATTCAGATTAAGAGTTTTCGATGAAGACCGGGT 1164
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DB 301 CCATTTACAGATGATGGATCAGATTTTCATCTGTGATCAAAAGAGAACTTCTACCT 360
QY 1165 GAAGTAGACACTAGTGAGAGATCTGCCATGTTAATACCCCAACACAAAGCGGTG 1224
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DB 361 GAAGTAGACACTAGTGAGAGATCTGCCATGTTAATACCCCAACACAAAGCGGTG 420
QY 1225 CTTGTACATCTTTGAACGCGGTTACGCGGAGAACTTAAAGAGTATGTTATGGGAATAT 1284
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DB 421 CTTGTACATCTTTGAACGCGGTTACGCGGAGAACTTAAAGAGTATGTTATGGGAATAT 480
QY 1285 CCG 1287
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DB 481 CCG 483

RESULT 2
R90192      559 bp      mRNA      linear      EST 30-Dec-1997
LOCUS      16347 Lambda-PRU2 Arabidopsis thaliana cDNA clone 191A617, mRNA
DEFINITION sequence.
ACCESSION  R90192
VERSION    R90192.1 GI:957732
KEYWORDS   EST.
SOURCE     thale cress.
ORGANISM   Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1 (bases 1 to 559)
AUTHORS   Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh
,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M., Retzel
,E. and Somerville,C.
TITLE      Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
JOURNAL    Plant Physiol. 106, 1241-1255 (1994)
MEDLINE    95148729
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COMMENT
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313ten@bm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
1..559
/organism="Arabidopsis thaliana"
/strain="var Columbia"
/db_xref="taxon:3702"
/clone="191A617"
/clone_lib="Lambda-PRU2"
/note="Vector: lambda Zip-Lox; Site 1: Sal; Site 2: Not;
Lambda PRU2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda Zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dt primed cDNA."
BASE COUNT   151 a  107 c  130 g  158 t  13 others
ORIGIN
Query Match      26.5%; Score 440.8; DB 14; Length 559;
Best Local Similarity 95.1%; Pred. No. 1.le-118;
Matches 451; Conservative 0; Mismatches 23; Indels 0; Gaps 0;
QY 805 GGAGATCATGATAAGATGTTCTTCTGTGAAGGAGACCAACATTCATCGGGAAGTCCCT 864
|||||
DB 1 GGAGATCATGATAAGATGTTCTTCTGTGAAGGAGACCAACATTCATCGGGAAGTCCCT 60
QY 865 TGGTTGATGTTTAAACAGACAATFACATTTGTTCCATCTCTGTGGTTAATACCGGTTTC 924
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DB 61 TGGTTGATGTTTAAACAGACAATFACATTTGTTCCATCTCTGTGGTTAATACCGGTTTC 120
QY 925 GATGATGAACAAAGCTATTCACAGAAAGCGGCTGCTTTCATCAGTATAGTAGG 984
|||||
DB 121 GATGATGAACAAAGCTATTCACAGAAAGCGGCTGCTTTCATCAGTATAGTAGG 180
QY 985 TATCTTTTTCACCAACTAATCCAAAGTATGGGCTTAGTCAGTATAGTACGAGGTTAC 1044
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DB 181 TATCTTTTTCACCAACTAATCCAAAGTATGGGCTTAGTCAGTATAGTACGAGGTTAC 240
QY 1045 TTATCGATCGGGATGAGAGATTTGGGATTCAGATTAAGAGTTTTCGATGAAGACCGGGT 1104
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DB 241 TTATCGATCGGGATGAGAGATTTGGGATTCAGATTAAGAGTTTTCGATGAAGACCGGGT 300
QY 1105 CCATTTACAGATGATGGATCAGATTTTCATCTGTGATCAAAAGAGAACTTCTACCT 1164
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DB 301 CCATTTACAGATGATGGATCAGATTTTCATCTGTGATCAAAAGAGAACTTCTACCT 360
QY 1165 GAAGTAGACACTAGTGAGAGATCTGCCATGTTAATACCCCAACACAAAGCGGTG 1224
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DB 361 GAAGTAGACACTAGTGAGAGATCTGCCATGTTAATACCCCAACACAAAGCGGTG 420
QY 1225 CTTGTACATCTTTGAACGCGGTTACGCGGAGAACTTAAAGAGTATGTTATGGG 1278
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DB 421 CTTGTACATCTTTGAACGCGGTTACGCGGAGAACTTAAAGAGTATGTTATGGG 474
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LOCUS      AV805720 RAPL9 Arabidopsis thaliana cDNA clone RAPL09-43-D18 3',
DEFINITION mRNA sequence.
ACCESSION  AV805720
VERSION    AV805720.1 GI:19830705
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LOCUS      AV805720 RAPL9 Arabidopsis thaliana cDNA clone RAPL09-43-D18 3',
DEFINITION mRNA sequence.
ACCESSION  AV805720
VERSION    AV805720.1 GI:19830705
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EST. thale cress.
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1 (bases 1 to 416)
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.

FEATURES
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/db_xref="taxon:3702"
/clone="RAF109-43-P18"
/clone_lib="RAFL9"
/dev_stage="plants at various developmental stages from
germination to mature seeds"
/lab_host="DH10B"
/note="Site.1: BamHI; Site.2: SalI; subjected to
dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24
hr) treatments"
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ORIGIN

Query Match 19.9%; Score 331; DB 10; Length 416;
Best Local Similarity 100.0%; Pred. No. 2.5e-86;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 416 AGGTATCAGACAGACCAGAAAAGATGCATATGGCAAGCTCTTCGGGAAATGTATCT 357
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QY 1392 TTTGAGTTTCACAGATAATCTGTGCAAGTGCTTGGTCTACATTTGGATGTAGCTCA 1451
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Db 356 TTTGAGTTTCACAGATAATCTGTGCAAGTGCTTGGTCTACATTTGGATGTAGCTCA 297
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QY 1452 AGGTCCTTGGAGGTTTAAGCGCTTCGATACCTCTATAGACCCGAAACCGTACAACTCCCGA 1511
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Db 296 AGGTCCTTGGAGGTTTAAGCGCTTCGATACCTCTATAGACCCGAAACCGTACAACTCCCGA 237
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QY 1512 TCCCTCGTGTGGTCGGCTATGTCGATGGAGCCCTGTGTTCCACTCGCCTCCATCTATGA 1571
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Db 176 TTGTTAAACGGAACGGGTATGACACGGGAACACTAGTTCCCTCATGTGAGACATTGTGA 117
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QY 1632 GGATATCAGCTGGGCACTTAAAGCTAGTATGA 1662
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Db 116 GGATATCAGCTGGGCACTTAAAGCTAGTATGA 86
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B77193

LOCUS	B77193	668 bp	DNA	linear	GSS 16-JAN-1999
DEFINITION	T31J1TR TAMU Arabidopsis thaliana genomic clone T31J1, DNA sequence.				
ACCESSION	B77193				
VERSION	B77193.1	GI:2773832			
KEYWORDS	GSS,				
SOURCE	thale cress.				
ORGANISM	Arabidopsis thaliana				
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.				
REFERENCE	1 (bases 1 to 668)				
AUTHORS	Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Adams,M.D. and Venter,J.C.				
TITLE	A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 3				
JOURNAL	Unpublished (1997)				
COMMENT	Other_GSSs: T31J1TR Contact: Steve Rounsley Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: rounsley@tigr.org Seq primer: M13 Reverse Class: BAC ends High quality sequence stop: 668.				
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Matches 430;	Conservative	0;	Mismatches 164;	Indels 12;	Gaps 1;
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Db	63	TGTTGGTGAATGCAGATACATTTGTGTGGATTTGTGTTATGGGCTAGAAACAAGACT	122		
QY	546	TTCTTAGCTCGGTTTTCTTTTACGGCGCTTTTAACGGATAGACTCTGCTGTTTGACCG	605		
Db	123	TACTTCTGCTTCTCTGTTTCTCTATGTCTCTTGTACTGACAGATCATGCTGTTGTACCA	182		
QY	606	AGGAAAGACATGATGATCTCTTTTCGAGCGCGTTTCTCGGTATGTCGTTGTGCTACC	665		
Db	183	ACGTACGACATAGTGAACCTTCTCTGTAGCCCTTTCCAGGTACTTCTCGGCTACTCCC	242		
QY	666	TTTAGATTTCCCTATGACTGATCATAGTTTGATGGATTAAATCAAGAATCATCTCGTTGTTA	725		
Db	243	TCTGGATTTTCCCACTAACAGATCAATTAGATAGCTTCAACAAGGAATCTCCGCGCTGTA	302		
QY	726	TGGATATATGGTGAAGAAATCAGGTGATTGATGATGATGACGGAAC-----TTTGTC	773		
Db	303	CGGAACAATGTTGAAGAATCATGTCATTAACCTAACACACAGAAAGCATCATCCCTC	362		
QY	774	TCATCTTTACTCTCTGTTTCATGATGATGAGATCATGATAGATGTTCTTCTCTGTA	833		
Db	363	GTACCTCTGCTTTATCTTATTCACGATACGACGATATGATGAAGATGTTCTTCTGTGA	422		
QY	834	AGGAGACCAACATTCATCGGAAAGTCCCTTGGTTGATTGTTAAAAACAGACAATTACTT	893		
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QY 884 TGTTCATCTCTGTGTTTAAATCCCGGTTTTCAGTATGATGAACAAAGCTATTCACCA 953
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DB 483 TATCCCATCTCTATGTTGATCCCTCTCTTTTCAGTCAGAATTAAAGCAAGCTATTCACCA 542

QY 954 GAAAGGAGCTGCTTTCATCAGTATGAGTATCTTTTTCACCCCAACCAAGATG 1013
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QY 1074 TCAAGT 1079
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DB 663 TCAAGT 668

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DEFINITION 30519 Lambda-PRL2 Arabidopsis thaliana cDNA clone 191A6XP 3', mRNA
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ACCESSION AA605483
VERSION AA605483.1 GI:2446011
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 507)
Newman,T., deBruijn,F.J., Green,P., Keegstra,K., Kende,H., McIntosh
,L., Ohlrogge,J., Raikhel,N., Somerville,S., Thomasow,M., Retzel
,E. and Somerville,C.
Genes galore: a summary of methods for accessing results from
large-scale partial sequencing of anonymous Arabidopsis cDNA clones
Plant Physiol. 106, 1241-1255 (1994)
95148729
Contact: Thomas Newman
MSU-DOE Plant Research Laboratory
Michigan State University
MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
Lansing, MI
Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcneibm.cl@msu.edu
The sequence entry for this EST has been reverse complemented and
is being submitted in the sense orientation.
Seq primer: M13 -21 dye primer.
FEATURES
Location/Qualifiers
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/clone_lib="Lambda-PRL2"
/note="Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
day germinated etiolated seedlings; 2) tissue culture
grown roots; 3) staged plants half with 24 hour light
cycle, half on 16 hr light, 8 hour dark- rosettes; 4)
same plants as 3 but aerial tissue (stems, flowers and
siliques. The vector is BRL's lambda zip-Lox. The cDNA
inserts were directionally cloned with Sal-Not arms using
oligo dT primed cDNA."
BASE COUNT 120 a 103 c 114 g 155 t 15 others
ORIGIN
Query Match 17.8%; Score 296; DB 9; Length 507;
Best Local Similarity 99.0%; Pred. NO. 5.6e-76;
Matches 296; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1364 ATGCCAAAGCTCTTGGGAAATATCTATCTTTTGAGTTTGACAGATAATCTTGTGCAAGTG 1423
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DB 123 ATGCCAAAGCTCTTGGGAAATATCTATCTTTTGAGTTTGACAGATAATCTTGTGCAAGTG 182

QY 1424 CTTGGTCTAGATTGGATATGTAGCTCAAGGTCTTGGAGGTTTAAAGCCTTGGATCTCT 1483
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 183 CTTGGTCTAGATTGGATATGTAGCTCAAGGTCTTGGAGGTTTAAAGCCTTGGATCTCT 242

QY 1484 ATACACCCGAAACCGTACAACTCCCGCATCTTCCTGCTGCTGGGCTATCTCCGATGAGC 1543
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 243 ATAGACCCGAAACCGTACAACTCCCGCATCTTCCTGCTGCTGGGCTATCTCCGATGAGC 302

QY 1544 CTTGTTTCCACTCGCTCCCATTTCTATGATGTTAAAGCGAAACCGGATTCACACGCGAA 1603
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 303 CTTGTTTCCACTCGCTCCCATTTCTATGATGTTAAAGCGAAACCGGATTCACACGCGAA 362

QY 1604 CACTAGTTCCTCATGTGAGACATTTGTGAGGATATCAGCTGGGACTTAAGCTAGTATGA 1662
  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 363 CACTAGTTCCTCATGTGAGACATTTGTGAGGATATCAGCTGGGACTTAAGCTAGTATGA 421

RESULT 6
LOCUS BE319670 645 bp mRNA linear EST 14-JUL-2000
DEFINITION NF017D12RT1094 Developing root Medicago truncatula cDNA clone
NF017D12RT 5', mRNA sequence.
ACCESSION BE319670
VERSION BE319670
KEYWORDS EST.
SOURCE baritel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 645)
Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May
,G.D. and Feiva,N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula root library
Unpublished (2000)
Contact: Palva NL
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7317
Fax: 580 221 7380
Email: nlpalva@noble.org
Medicago Genome Initiative accession: MGI:S:16402
Insert Length: 645 Std Error: 0.00
Plate: 017 ROW: D Column: 12
Seq primer: TCACACAGGAACACGCTATGAC.
Location/Qualifiers
source
1. 645
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF017D12RT"
/clone_lib="Developing root"
/issue_type="root"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Total RNA was extracted from
non-modulated roots of plants grown in 1 mM nitrate
medium. Samples were taken at four time points
(approximately two days, one, two and six weeks post
germination) representing early seedling growth to
nitrogen limitation."
BASE COUNT 184 a 139 c 111 g 211 t
ORIGIN
Query Match 16.9%; Score 281; DB 10; Length 645;
Best Local Similarity 64.9%; Pred. No. 1.6e-71;

```

Matches 416; Conservative 0; Mismatches 225; Indels 0; Gaps 0;		FEATURES		Location/Qualifiers	
		source		1..597	
				/organism="Lotus japonicus" /cultivar="Gifu (B-129)" /db_xref="taxon:34305" /clone_lib="Lotus japonicus nodule library, mature and immature nodules" /note="Organ: Nodule; Vector: pBluescript SK-; Site: 1: EcoRI; Site: 2: XhoI; The library was prepared using mRNA extracted from a mixture of mature (pink) and immature (white) nodules of Lotus japonicus ecotype 'Gifu'. Nodules were induced by, and contained Mesorhizobium loti strain NZP2235."	
BASE COUNT		176 a	112 c	131 g	177 t
ORIGIN		1 others			
Query Match		16.8%; Score 280; DB 13; Length 597;			
Best Local Similarity		66.9%; Pred. No. 3.1e-71;			
Matches 397; Conservative		0; Mismatches 196; Indels 0; Gaps 0;			
QY	856	AAAGTCCCTTGGTTGATTGTTAAACACAGACAATTACTTTCTTCATCTCTCTGGTTAATA	915		
DB	5	AAAGTACCTTGGTTAGTGTAGTGAACAAACAGATAATTTTCGTTCCATCTCTATTTCTTGATG	64		
QY	916	CCGGGTTTCGATGATGAACATAACAAAGCTATTCACAGAAAGGAGCTGTCTTTTCATCAC	975		
DB	65	CCATCTTATCAGCAGGAACCTGAATGATCTCTTCCCAAGAAAGCAACAGGTTCCATTTTC	124		
QY	976	TTAGGTAGGTATCTTTTTCACCAACTAACCAAGTATGGGGCTTTAGTCACTAGATACTAC	1035		
DB	125	TTGGGTAGATATATGCTCCACCCACAAACAATGTGTGGGACTTGTGTGCAGATACTAT	184		
QY	1036	GAAGCTTACTTATCGCATCGGATGAGAAGATTCGGGATTCGAAGTAAGAGTTTCGATGAA	1095		
DB	185	CAAGCTTATTTAGCTAAAGTTGATGAAAGAGTAGGCATACAAATTAGAGTGTTTGTCCA	244		
QY	1096	GACCCGGTCCATTTTCAGCATGTGATGGATCAGATTTTCATCTTGTACTCAAAAAGAGAAA	1155		
DB	245	GAACCTGGTCCATTTCAACATGTTCTGGATCAGATCTTAGCTTGTACTTTTGAAGGAGAA	304		
QY	1156	CTTCTACCTGAAGTAGACACACTAGTGGAGAGATCTCGCCATGTTTAAATACCCCAACAC	1215		
DB	305	CTTTTACCCGATGTTGACCGTGAGCAGCAATAATATTAGTTTCATCTGGACTACCAAGTCA	364		
QY	1216	AAAGCCGTGCTGTGCATCTTTTGAACCGGGTTTACCGGAGAACTTTAAAGAGTATGTAT	1275		
DB	365	AAAGCTGTGCTCATGACATCTTTAAGCTCTGGTTATTTTGAAGAGGTAAGAGACATGTAT	424		
QY	1276	TGGGAATATCCGACATCAACTGGAGAAATCATCGGTGTTTCATCAGCCGAGCCCAAGAGGT	1335		
DB	425	TGGGAGTATCTTACCGTGACAGGAGAAAGTGTGCGGGCTTTTCCAGCCCAAGCCATGAAG	484		
QY	1336	TATCAGCAGACCCGAAAAAGATGCATAATGGCAAAAGCTCTTGGGAAATGTATCTTTTG	1395		
DB	485	TATCAGCAAAAGCAGAGAGAGATGCACAACTTAAAGCTTGGNCAGAAATGTATCTCTTA	544		
QY	1396	AGTTTTCACAGATAATCTTGTGCAAGTGTCTTGGTCTACATTTGGATATGTAGC	1448		
DB	545	AGCTTAACAGACGTGTGGTTACTAGTCTGCTGCTACTTTTGGCTATGTGGC	597		
RESULT 8		AV807820/c			
LOCUS		AV807820			
DEFINITION		mRNA sequence.			
ACCESSION		AV807820			
VERSION		AV807820.1			
KEYWORDS		EST.			
SOURCE		thale cress.			
ORGANISM		Arabidopsis thaliana			
REFERENCE		Arabidopsis thaliana			
AUTHORS		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
TITLE		Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
JOURNAL					
COMMENT					


```

Db 545 AGCTTACACA 555

RESULT 10
B23728
LOCUS
DEFINITION
F16M20TR IGF Arabidopsis thaliana genomic clone F16M20, DNA
sequence.
ACCESSION
B23728.1 GI:2509359
VERSION
B23728
KEYWORDS
GSS.
SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 671)
Rounsley,S.D., Field,C.E., Bass,S., Linher,K., Coffey,E., Golden,K.
, Johnson,K., Adams,M.D. and Venter,J.C.
A BAC End Sequence Database for Identifying Minimal Overlaps in
Arabidopsis Genomic Sequencing
Unpublished (1997)
Other_GSSs: F16M20TFB
Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounsley@tigr.org
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 671.
FEATURES
Source
1..671
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="F16M20"
/clone_lib="IGF"
/notes="hermaphrodite"
/sex="Vector: BelobACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
BASE COUNT 184 a 144 c 139 g 204 t
ORIGIN
Query Match 15.6%; Score 259.6; DB 17; Length 671;
Best Local Similarity 66.7%; Pred. No. 3.4e-65;
Matches 408; Conservative 0; Mismatches 189; Indels 15; Gaps 2;

QY 268 GATAAGCTTCTCGAGGGCTACTTGGTCTTCTGTTTTCATGAAGATTCTTGCCTTAGTAGG 327
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 GATAGACTAATAGGAGGCGCTTTTAACCGCAGATTTCGATGAAGTTCTTGGTCAGTAGG 119
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 328 TACC---AATCAGTTCATTAACCGTAAACCTTCACCTTACAGCATCTTCTTATCTCATC 384
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 TATCATAAACTTCTGTATCGCAGCCCTTACCATAACAGCGCTGTAATATCTTGTC 179
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 385 TCTAAGCTTAGAACTACGAAAGCTTTCACAAGCGATGTGTCGGGTACTGAATCTTAC 444
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 180 TCGAAGCTTAGAAGCTATGATAGCTTTCACAAAGTTTGGCTCCAGGACAAAGCTTAC 239
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 445 AAGAAAGCTTAAACACACTTGATCAAGACATATTGATGGT-----GATGGT 492
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 240 AAGGAAGACAACAAGCATCTTACTCATGATGAGAATTAATGAACGAATAATCATGGT 299
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY* 493 GAATGCAATATGTTGTGATTTCTTTTAGCGGCTTAGGACAGATATCTTCTCTA 552
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 300 GAATGCCGATACGTTGTGTGCGTGCCTGATTAACCGGCTTGAACACCGACTACTCACTTT 359
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 553 GCCTCGGTTTTCTTTACCGGCTTTTAAACGGATAGAGTCTTGTGTTGACCGAGGAAA 612
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 360 GCTTCTGTGTTCTCTACGCTCTTCTGACTGATAGATCATCTTGTGTGACACCGCAAG 419
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY 613 GACATGGATGATCTCTTTTTCGAGCCGTTTCTCGTATGTCGTTGTTGCTACCTTTAGAT 672
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 420 GATATTGGTGATCTCTATGCGAGCCATTTCAGGTACTTCTGTTGTTCTCTCTCGAC 479
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 673 TTCCTATGACTGATCAGTTTTCATGATTAATCAAGATCATCTCGTTGTTATGGATAT 732
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 480 TTTCCATTGATGAATATGCTGATGATACCAACAGGGATCTCTGTTGTTACGAACA 539
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 733 ATGGTGAACAATCAGGTGATGATGATGAGGAACTTTTCTCATCTTTTATCTTCATCTT 792
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 540 ATGTTGGAAATCATTCATCAACTCGATTCATTCCCGCCCATCTATATAGGCATAAC 599
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 793 GTTCATGATATTGAGAGATCATGATAAGATGTTCTTCTGTGAAGAGACAAACATCATC 852
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 600 CTTTCATGATTCAGGAGTAGTATAGATGTTCTTCTGCAAAAGATCAAAAGTTTGATT 659
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 853 GGGAAAGTCCCT 864
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 660 GACAAAGTCCCT 671
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
BF597909
LOCUS
DEFINITION
BF597909.1 GI:11690303
Gm-cl056-656 5' similar to TR:081052 081052 T18E12.11 PROTEIN. [1]
; mRNA sequence.
ACCESSION
BF597909
VERSION
BF597909.1 GI:11690303
KEYWORDS
EST.
SOURCE
soybean.
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
1 (bases 1 to 508)
Shoemaker,R., Kelm,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna
,A., Holla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
,R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccufesgen.com
Insert Length: 796 Std Error: 0.00
High quality sequence stop: 411.
FEATURES
Source
1..508
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl056-656"
/clone_lib="Gm-cl056"
/tissue_type="Whole seedling, 4 day old"
/lab_host="DH10B"
/notes="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from 4 day old seedling of P1468916. The seedlings were
germinated in a growth chamber using germination paper.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with a XhoI restriction
site. EcoRI adapters were ligated to the blunt-ended cDNA

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fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in the laboratory of Dr. Randy Shoemaker."

BASE COUNT	140 a	104 c	131 g	132 t	1 others
ORIGIN					
Query Match	15.2%; Score 252.6; DB 12; Length 508;				
Best Local Similarity	72.3%; Pred. NO. 3.6e-63;				
Matches	327; Conservative	0; Mismatches	125; Indels	0; Gaps	0;
Qy	1207 CCCAACACAAAGCGTCTTGTTCACATCTTTTGACGCGGGTTACGCGGAGAACCTTAAAG 1266				
Db					
Qy	8 CCCAAGTCAAAAGCGGTACTGATGACATCCCTTAAACTCTGGTTATTTGAAAAGGTGACA 67				
Qy	1367 AGTATGATTTGGGATATCCGACATCAACTGCAGAAATCATCCCTGTTTCATCAGCGGACC 1326				
Db					
Qy	1327 CAAGAAGGTTATCAGCAGACCGAAAAAAGATGCATATGCGCAAGCTCTTCGGGAAATG 1386				
Db					
Qy	1387 TATCTTTTGTGTTTGCACAGATAATCTTGTGACAACTGCTTGGTCTACATTTTGGATATGTA 1446				
Db					
Qy	1447 CTTCAAGCTCTTGGAGCTTTAAAGCTTTCATATGATGATGATGATGATGATGATGATG 1506				
Db					
Qy	1507 CCGATCTCTTGTGTGGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1566				
Db					
Qy	1567 TATGATTGTTAAAGCGAAACGGGTATTGACAGCGGGAACACTAGTTTCCCTCATGTGAGACAT 1626				
Db					
Qy	1627 TGTGAGGATATGAGCTGGGGCTTAAAGCTTGT 1658				
Db					

RESULT 12
BF009322
LOCUS
DEFINITION
SS76g10.y1 Gm-cl064 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl064-91 5' similar to TR:081052 081052 T18E12.11 PROTEIN. [1]
; mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
BF009322
BF009322.1 GI:10709598
EST.
soybean.
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
glycine.
1 (bases 1 to 561)
Shoemaker,R., Kaim,P., Vodkin,L., Erdelding,J., Coryell,V., Khanna
A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
Wille,I., Underwood,K., Steptoe,M., Theising,B., Allen,N., Bowers
V., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
R., Ritter,E., Kohn,S., Shin,T., Jackson,V., Cardenas,M., McCann
R., Waterston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewartson.wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccluresgen.com
High quality sequence stop: 422.

FEATURES
LOCATION/Qualifiers
1..561
/organism="Glycine max"
/cultivar="Williams"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl064-91"
/clone_lib="Gm-cl064"
/tissue_type="seedling epicotyls"
/dev_stage="2 week old"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from the epicotyls of 2 week old seedling for the cultivar
Williams. The seedlings were germinated in a growth
chamber, excised above the soil level, and the plants
were placed in a 100 ppm solution of auxin for 24 hours
prior to harvesting. Complementary DNA was synthesized
from mRNA using a primer consisting of a poly(dT)
sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed
by XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into DH10B host cells (GibcoBRL). This
library was constructed in the laboratory of Dr. Randy
Shoemaker."

BASE COUNT	137 a	112 c	109 g	202 t	1 others
ORIGIN					
Query Match	15.1%; Score 250.2; DB 12; Length 561;				
Best Local Similarity	67.0%; Pred. No. 1.9e-62;				
Matches	354; Conservative	0; Mismatches	174; Indels	0; Gaps	0;
Qy	493 GAATGCAATATGTTGTGTGGATTTCTTTTACGGCGTTTACGGCAACAGATACATTCTCTCA 552				
Db					
Qy	553 GCCTCGGTTTTTCTTTACGGCTTTTAAAGGATAGATCTTCTCTTGTGACCGAGGAAA 612				
Db					
Qy	613 CACATGGATGATCTCTTTTTCGAGCGCTTTTCTCGGTATGTCGGTGTGCTTACCTTTAGAT 672				
Db					
Qy	154 GATATGGTTGATCTCTTTTGTGAGCCATTCCAGATCTCTCTGGCTTCTCTAGTGAC 213				
Db					
Qy	673 TTCCCTATGACATGATCTTTCATGCGATTAAATCAAGATCAATCTCTTCTTATGATAT 732				
Db					
Qy	733 ATGGTGAAGATCAGGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 792				
Db					
Qy	274 ATGCTGAAAGTAAAGACACATGATGATGATGATGATGATGATGATGATGATGATGAT 333				
Db					
Qy	793 GTTTCATGATTATGAGATCATGATGATGATGATGATGATGATGATGATGATGATGAT 852				
Db					
Qy	853 GGGAAAGTCCCTTGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 912				
Db					
Qy	394 CAGATCGTCCCATGGTTATATGAAAAACAGATACTACTTTGTCCCTCTGTATTCTTA 453				
Db					
Qy	913 ATACCGGGTTTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 972				
Db					
Qy	454 ATGCCATCTTTTGAGCAGCAAGTGAATGATGATGATGATGATGATGATGATGATGATGAT 513				
Db					


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QY 973 CACTTAGTAGTATCTTTTCACCCCACTAACCAAGTATGGGCTTA 1020
Db 514 TTCTTGAGTAGGTATCTGTTCCACCCTACGAACAGTGTGTAGGACTA 561

RESULT 13
BE346170
LOCUS
DEFINITION
    BE346170
    sp19b08.y1 Gm-cl042 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
    Gm-cl042-976 5' similar to TR:081052 081052 T18E12.11 PROTEIN. ;
    mRNA sequence.
ACCESSION
    BE346170
VERSION
    BE346170.1 GI:9257961
KEYWORDS
    EST.
SOURCE
    soybean.
ORGANISM
    Glycine max
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
    Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
    Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
    Glycine.
REFERENCE
    1 (bases 1 to 605)
    Shoemaker,R., Keim,P., Vodkin,L., Erpelting,J., Corvett,V., Khanna
    A., Bolla,B., Marrà,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
    Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
    X., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
    R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
    R., Waterston,R. and Wilson,R.
    Public Soybean EST Project
    Unpublished (1999)
    Contact: Shoemaker R/Public Soybean EST Project
    Public Soybean EST Project
    Washington University School of Medicine
    4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
    Tel: 314 286 1800
    Fax: 314 286 1810
    Email: est@watson.wustl.edu
    This clone is available through: ResGen, Invitrogen Corp. 2130
    South Memorial Parkway Huntsville, AL 35801 For further information
    call: (800)-533-4363 or contact via email: ccu@resgen.com
    High quality sequence stop: 460.
FEATURES
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        /db_xref="taxon:3847"
        /clone="GENOME SYSTEMS CLONE ID: Gm-cl042-976"
        /clone_lib="Gm-cl042"
        /tissue_type="Whole seedling without cotyledons"
        /note="Vector: pBluescriptII SK+; Site.1: EcoRI; Site.2:
        XhoI; This cDNA library was constructed from mRNA isolated
        from 2 week old seedlings with the cotyledons removed at
        the time of harvest. The seedlings for the cultivar Raiden
        were grown in a growth chamber using germination paper.
        Complementary DNA was synthesized from mRNA using a primer
        consisting of a poly(dT) sequence with a XhoI restriction
        site. EcoRI adapters were ligated to the blunt-ended cDNA
        fragments followed by XhoI digestion. The cDNA fragments
        were directionally cloned into the EcoRI-XhoI restriction
        site of the pBluescript vector. The ligated cDNA fragments
        were transformed into DH10B host cells (Gibco BRL). This
        library was constructed by Dr. Randy Shoemaker."
BASE COUNT 175 a 118 c 126 g 184 t 2 others
ORIGIN
    Query Match 14.8%; Score 245.2; DB 10; Length 605;
    Best Local Similarity 65.5%; Pred. No. 5.8e-61;
    Matches 372; Conservative 0; Mismatches 195; Indels 1; Gaps 1;

QY 772 TCTCATCTTTATCTTCTGTTTCATGATATGAGATCATGATGATGTTCTTCTGT 831
Db 36 TCTTTTGTCTACCTTCATATAGCCCATGATGATGATGATGATGATGATGATGAT 95

QY 832 GAAGGAGACCAACATTCATCGGGAAGCTCCCTTGTTGATTGTTAAACAGACAAATTAC 891

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Db 96 GATGAAGAACAACGTTTCTCCAGATCGTGCCCTTAATATGAACAGATAACTAC 155
QY 892 TTGTGTTCCATCTCTGTTGTTAATACCGGGTTTCGGATGATGAACAAAGCTATTCCCA 951
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QY 1252 GCGGAGAACTTAAAGAGTATGTTGGGAATATCCGACATCACTGGAGAAATCATCGGT 1311
Db 516 TTGAAAGGTGAGAGACATGATTTGGGAATATCTTACNGTACNGGAGGAGTGGGTGGC 575
QY 1312 GTTCATCAGCGGAGCAACAGGTTATC 1339
Db 576 GTT-ACCAGCCGAGCCCGCAAGATTTC 602

RESULT 14
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    mRNA sequence.
ACCESSION
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VERSION
    AV831440.1 GI:19873500
KEYWORDS
    EST.
SOURCE
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ORGANISM
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    Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
    1 (bases 1 to 314)
    Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
    Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
    Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
    and Shinozaki,K.
    Large scale analysis of Arabidopsis full-length cDNA (2002b)
    Unpublished (2002)
    Contact: Motoaki Seki
    Plant Functional Genomics Research Group
    RIKEN Genomic Sciences Center
    3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
    Tel: 81-298-36-4359
    Fax: 81-298-36-9060
    Email: mseki@rtc.riken.go.jp
    An Arabidopsis full-length cDNA library was constructed essentially
    as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
    and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
    al., submitted for publication) digested with BamHI and SalI. This
    clone is in a modified pBluescript vector. Please visit our web
    site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
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FEATURES
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Best Local Similarity 96.5%; Pred. No. 3.1e-58;
Matches 250; Conservative 0; Mismatches 7; Indels 2; Gaps 1;

QY 1 ATGGATCAGATTCTACAGGAGAGATCGTCTCCGATCAGAACCACT--ACCGGGGGTT 58
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QY 59 CAAGTCGCTTAATTTCTCCGAACTACTTCAAAATGAAGTATCTCAGTCCGGTACCATCA 118
DB 116 CAAGTCGCTTAATTTCTCCGAACTACTTCAAAATGAAGTATCTCAGTCCGGTACCATCA 175
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DB 176 AGCTCAGAGAACCTTCACTACTTGCCTTGATAGTCTCTCTGATAGTACGATTCCTCAA 235
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RESULT 15
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ACCESSION  B18679
VERSION    B18679.1 GI:2316583
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Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 786)
Feng,J., Dewar,K., Buehler,E., Kim,C., Li,V., Shinn,P., Sun,H. and
Ecker,J.
BAC End Sequences at ATGC
Unpublished (1997)
Other GSSs: F16A14-sp6
Contact: Ecker J
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Pennsylvania, Philadelphia, PA
19104
Tel: 215-898-9384
Fax: 215-898-8780
Email: jecker@atgenome.bio.upenn.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 64
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/db_xref="taxon:3702"

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Produced by Thomas Altmann"
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Matches 371; Conservative 0; Mismatches 210; Indels 4; Gaps 2;

QY 1054 GCGGATCAGACAGATTGGGATTAAGTATTCATGAAGACCGGGTCCATTTCAG 1113
DB 715 GCGGAGGAGGNGGTATTATAGAGAAGGGGTAGTTTCAGCATTCGAGGGGAAATNTAA 656
QY 1114 CATGTGATGATCAGATTTTCATCTTGTACTCAAAACACAGAAATTCACCTGAGTAGAC 1173
DB 655 CAGGNAAGGATCAAGTTGTAACTTGGACAGGAAGAGAG--ACCTTTTGCCTGAACAGGT 597
QY 1174 ACACATAGTGGAGAGATCTGCG---CATGTTAATACCCCAACACAAAGCGCTTGTC 1230
DB 596 GCACAAGAGAGCCAAAGATCATATATCAAGAAAGCCAGACACTTANAGCTGTTCTNGTC 537
QY 1231 ACATCTTTTCAACCGCGGTTACGCGGAGAACTTAAAGAGTATGTTTGGGAATATCCGACA 1290
DB 536 ACATCTTTTNGTATCCAGAGTACTCTGANACCTTANAGAAGCATGTTTGGGAACGCCAGT 477
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DB 416 AGCAAGTACACCAACCAAGGCGCTCGCGGAGANGTATCTTCTAGTCTTACTGTATTA 357
QY 1411 CTTGTGACAAAGTCTTTGGTCTACATTTGGATATGATGATCAAGGTCTTGGAGGTTAAAG 1470
DB 356 ATAGTCACAAGTCAAGGCTACATTTNGGATATGTTCTCATATTTCTTCCAGCATTAAG 297
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DB 296 CCATGTTTACTTTATCAGCCAGCAGGTCTGATACAGTCTCTGATCCAGAGNGTATTCAATCC 237
QY 1531 ATGTCGATGAGCGCTTTTTCACCTCGCTCCATTCATCATCTTAAAGCGAAACCGCT 1590
DB 236 AGCTGATGAGCAATTCATGTCAGTATGAGACATTGTGAGAT 1635
QY 1591 ATTGACACGGGAACTAGTTCCTCATGTGAGAGACATTGTGAGAT 177
DB 176 ACTAAGTCCGGGAAGTACTTCTCTGNGAAGCATTCGACGAT 132

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Job time : 2208 secs